

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 15:46:56 ; Search time 210.42 Seconds
(without alignments)
7.313 Million cell updates/sec

Title: US-09-331-631a-1_COPY_29_73
Perfect score: 252
Sequence: 1 SEFDROXYECCRQCMQLET.....RCVSQCDKRFEDIDMSKYD 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_36:*

1:	/SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT:*
2:	/SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT:*
3:	/SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT:*
4:	/SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT:*
5:	/SIDSL/gcgdata/geneseq/geneseq/AA1984.DAT:*
6:	/SIDSL/gcgdata/geneseq/geneseq/AA1985.DAT:*
7:	/SIDSL/gcgdata/geneseq/geneseq/AA1986.DAT:*
8:	/SIDSL/gcgdata/geneseq/geneseq/AA1987.DAT:*
9:	/SIDSL/gcgdata/geneseq/geneseq/AA1988.DAT:*
10:	/SIDSL/gcgdata/geneseq/geneseq/AA1989.DAT:*
11:	/SIDSL/gcgdata/geneseq/geneseq/AA1990.DAT:*
12:	/SIDSL/gcgdata/geneseq/geneseq/AA1991.DAT:*
13:	/SIDSL/gcgdata/geneseq/geneseq/AA1992.DAT:*
14:	/SIDSL/gcgdata/geneseq/geneseq/AA1993.DAT:*
15:	/SIDSL/gcgdata/geneseq/geneseq/AA1994.DAT:*
16:	/SIDSL/gcgdata/geneseq/geneseq/AA1995.DAT:*
17:	/SIDSL/gcgdata/geneseq/geneseq/AA1996.DAT:*
18:	/SIDSL/gcgdata/geneseq/geneseq/AA1997.DAT:*
19:	/SIDSL/gcgdata/geneseq/geneseq/AA1998.DAT:*
20:	/SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT:*
21:	/SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	252	100.0	666	19 W62828	Macadamia integrif
2	252	100.0	666	19 W62829	Macadamia integrif
3	180	71.4	625	19 W62830	Macadamia integrif
4	78.5	31.2	590	19 W62832	Gossypium hirsutum
5	70.5	28.0	525	19 W62831	Theobroma cacao an
6	70.5	28.0	566	13 R20181	Sequence encoded b
7	67	26.6	218	19 W40287	Human TSPI protein
8	67	26.6	218	20 Y06182	Thrombospondin I f
9	67	26.6	239	14 R40823	Human thrombospond
10	67	26.6	441	19 W40288	Human concatamers
11	67	26.6	441	20 Y06183	Thrombospondin I f
12	63	25.0	444	20 W90340	G. max truncated S

13	63	25.0	524	20 W90339	G. max SBP1 protei
14	62.5	24.8	409	20 W90342	G. max truncated S
15	62.5	24.8	489	20 W90341	G. max SBP2 protei
16	62	24.6	941	21 Y66736	Membrane-bound pro
17	59.5	23.6	2703	16 R70236	P. falciparum Proj
18	59.5	23.6	2710	18 W22482	P. falciparum Proj
19	59.5	23.6	2710	21 Y77904	P. falciparum Proj
20	59.5	23.6	3060	21 W22475	Plasmodium var-7
21	59.5	23.6	3060	21 Y77905	Plasmodium var-7 p
22	57	22.6	1284	9 P81187	Sequence encoded b
23	56.5	22.4	593	19 W62835	Zea mays antimicro
24	55	21.8	623	20 W30622	Arabidopsis enhanc
25	55	21.8	816	16 R85870	WD-40 domain-contg
26	53.5	21.2	450	19 W56779	Human beclin prote
27	53.5	21.2	450	19 W56784	Human beclin prote
28	53	21.0	35	13 R21079	Antimicrobial maiz
29	52.5	20.8	569	20 Y24054	A human beta-trans
30	52.5	20.8	569	21 Y83041	F-box protein FBP-
31	52.5	20.8	569	21 Y83250	F-box protein hbet
32	52.5	20.8	569	21 Y44249	Human cell signal
33	52	20.6	33	19 W62836	Zea mays antimicro
34	52	20.6	58	20 Y32115	Maize id gene NslI
35	52	20.6	436	20 Y32114	Maize id protein.
36	52	20.6	623	20 W30620	Arabidopsis La-er
37	52	20.6	623	20 W30624	Arabidopsis mutant
38	51.5	20.4	147	13 R22950	Leech antiplatelet
39	51.5	20.4	569	21 Y83254	F-box protein FWD1
40	51.5	20.4	5250	21 Y53678	Sequence g1/442661
41	49.5	19.6	98	17 R91700	AcANP6. Ancylost
42	49.5	19.6	98	20 Y30395	Nematode extracted
43	49.5	19.6	562	18 W12096	Adenovirus E1a ass
44	49	19.4	411	21 Y77914	Plasmodium DBL gen
45	49	19.4	467	21 Y70814	Extended human zsl

ALIGNMENTS

RESULT	1
ID	W62828
XX	W62828 standard; Protein; 666 AA.
XX	
AC	W62828;
XX	
DT	27-OCR-1998 (first entry)
XX	
DE	Macadamia integrifolia antimicrobial protein.
XX	
KW	antimicrobial protein; infestation; control.
XX	
OS	Macadamia integrifolia.
XX	
FH	Key
FT	Peptide
FT	Location/Qualifiers
FT	1..28
FT	/note= "signal peptide"
FT	29..666
FT	/note= "mature protein"
XX	
PN	W09827805-A1.
XX	
PD	02-JUL-1998.
XX	
PF	22-DEC-1997: 97WO-AU00874.
XX	
PR	20-DEC-1996: 96AU-0004275.
XX	
PA	(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
XX	
PI	Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
XX	
DR	WPI: 1998-377279/32.
XX	
DR	N-PSDB: V42310.
XX	

PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
XX useful for controlling microbial infestations of plants or mammals
XX
PS Claim 1; Page 34-36; 96pp; English.
XX
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
XX
SQ Sequence 666 AA;

Query Match 100.0%; Score 252; DB 19; Length 666;
Best Local Similarity 100.0%; Pred. No. 2.3e-23;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEPDRQYECKRCQCMQLETSQGMRCVSOCDKRFEDIDWSKYD 45
Db 29 sefdrgyeckrqcmqltsgqmrvcsgcdkrfeedidwskyd 73

RESULT 2
ID W62829 standard; Protein; 666 AA.
XX
AC W62829;
XX
DT 27-OCT-1998 (first entry)
XX
DE Macadamia integrifolia antimicrobial protein.
XX
KM antimicrobial protein; infestation; control.
XX
OS Macadamia integrifolia.
XX
FH Key Location/Qualifiers
FT Peptide 1..28 /note= "signal peptide"
FT Protein 29..666 /note= "mature protein"
XX
PN W09827805-A1.
XX
PD 02-JUL-1998.
XX
PF 22-DEC-1997; 97WO-AU00874.
XX
PR 20-DEC-1996; 96AU-0004275.
XX
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
XX
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
XX
DR WPI; 1998-377279/32.
XX
DR N-PSDB; V42311.
XX
XX Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
XX
PS Claim 1; Page 39-41; 96pp; English.
XX
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
XX
SQ Sequence 666 AA;

Query Match 100.0%; Score 252; DB 19; Length 666;
Best Local Similarity 100.0%; Pred. No. 2.3e-23;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEPDRQYECKRCQCMQLETSQGMRCVSOCDKRFEDIDWSKYD 45

Db 29 sefdrgyeckrqcmqltsgqmrvcsgcdkrfeedidwskyd 73

RESULT 3
ID W62830 standard; Protein; 625 AA.
XX
AC W62830;
XX
DT 27-OCT-1998 (first entry)
XX
DE Macadamia integrifolia antimicrobial protein.
XX
KM antimicrobial protein; infestation; control.
XX
OS Macadamia integrifolia.
XX
FH Key Location/Qualifiers
FT Peptide 1..28 /note= "signal peptide"
FT Protein 29..666 /note= "mature protein"
XX
PN W09827805-A1.
XX
PD 02-JUL-1998.
XX
PF 22-DEC-1997; 97WO-AU00874.
XX
PR 20-DEC-1996; 96AU-0004275.
XX
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
XX
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
XX
DR WPI; 1998-377279/32.
XX
DR N-PSDB; V42316.
XX
XX Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
XX
PS Claim 1; Page 43-45; 96pp; English.
XX
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
XX
SQ Sequence 625 AA;

Query Match 71.4%; Score 180; DB 19; Length 625;
Best Local Similarity 100.0%; Pred. No. 1.7e-14;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 QCMQLETSQGMRCVSOCDKRFEDIDWSKYD 45
Db 1 qcmqltsgqmrvcsgcdkrfeedidwskyd 32

RESULT 4
ID W62832 standard; Protein; 590 AA.
XX
AC W62832;
XX
DT 27-OCT-1998 (first entry)
XX
DE Gossypium hirsutum antimicrobial protein.
XX
KM antimicrobial protein; infestation; control.
XX
OS Gossypium hirsutum.

XX MO9827805-A1.
 PN 02-JUL-1998.
 PD
 XX
 XX 22-DEC-1997; 97WO-AU00874.
 PF
 XX 20-DEC-1996; 96AU-0004275.
 PR
 XX (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
 PA
 XX Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
 PI
 XX WPI, 1998-377279/32.
 DR
 XX
 XX Novel anti-microbial protein from e.g. Macadamia integrifolia -
 PT useful for controlling microbial infestations of plants or mammals
 PT
 XX
 XX Claim 1; Page 49-51; 96pp; English.
 PS
 XX
 XX The sequence is that of an antimicrobial protein which can
 CC be used to control microbial infestations in plants and mammalian
 CC animals.
 XX
 XX Sequence 590 AA;

	Query Match	31.2%	Score 78.5	DB 19	Length 590:
	Best Local Similarity	40.5%	Pred. No. 0.055:		
	Matches	15;	Conservative	9;	Mismatches 12; Indels 1; Gaps 1:
QY	2 EFDROEIECKRQCQMLETSGGMRCVCSGDKRFEDD	38			
	I : :: ::I : I : I : :				
Dh	81 eadpqriyeecqdecrqge-erqpapqcrcqlkrrfge	116			

XX	RESULT	5
XX	ID	W62831
XX		W62831 standard; Protein; 525 AA.
XX	AC	
XX		W62831;
XX	DT	27-OCT-1998 (first entry)
XX	DE	Theobroma cacao antimicrobial protein.
XX	KM	antimicrobial protein; Infestation; control.
XX	OS	Theobroma cacao.
XX	PN	WO9827805-A1.
XX	PD	02-JUL-1998.
XX	PF	22-DEC-1997; 97WO-AU00874.
XX	PR	20-DEC-1996; 96AU-0004275.
XX	PA	(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
XX	PI	Bower NT, Goulter KC, Green JL, Manners JM, Marcus JP;
XX	DR	WPI; 1998-377279/32.
XX	PT	Novel anti-microbial protein from e.g. Macadamia integrifolia -
XX	PT	useful for controlling microbial infestations of plants or mammals
XX	PS	Claim 1, Page 47-49; 96pp; English.
XX	CC	The sequence is that of an antimicrobial protein which can
XX	CC	be used to control microbial infestations in plants and mammalian
XX	CC	animals.

SQ	Sequence	525 AA;
	Query Match	28.0%, Score 70.5; DB 19; Length 525; Best Local Similarity 32.4%; Pred. No. 0.47; Matches 11; Conservative 11; Mismatches 11; Indels 1; Gaps 1;
OY	5 ROEVECKRQCQLLET-SGOMRRCVSQCDDREE	37 :: :: :: : : : : : : : : Db 39 rgyqyegcqrrcesateeregegcqcrcereyke 72

	RESULT	5
R20181		
ID	R20181	standard; Protein; 566 AA.
XX		
AC	R20181;	
XX		
DT	16-APR-1992	(first entry)
XX		
De	Sequence encoded by 67 kD T. cacao protein cDNA	
XX		
KW	Cocoa; flavour; vicillin; seed storage protein.	
XX		
OS	Theobroma cacao.	
XX		
PN	WO9119801-A.	

XX 26-DEC-1991.
PD
XX 07-JUN-1991; 91WO-GB00914.
PE
XX
PR 11-JUN-1990; 90GB-0013016.
XX
PA (MRSC) MARS UK LTD.
XX
PI
XX Spencer ME, Hodge R, Deakin EA, Ashlon S;
XX
WPL; 1992-024418/03.
DR N-PSDB; Q20377.
DR

PT Recombinant cocoa proteins - are responsible for flavour in cocoa
PT beans and produced in large quantities using yeast and bacterial
PT expression vectors
XX
XX
PS Claim 4; Fig 2; 59pp; English.
XX
CC The inventors claim a 67 kD and 31 kD T₁ cacao protein, and
CC fragments, and encoding DNAs. The 47 kD and 31 kD proteins are
CC derived from the 67 kD precursor. T₁ cacao protein cDNA was
CC detected in a cDNA library prepared from immature cocoa beans RNA
CC using a probe based on the AA sequence of a CNBR peptide common to
CC the 47 kD and 31 kD polypeptides. Homology searches revealed close
CC homologues between the 67 kD polypeptide and the vicillins, which are
CC seed storage proteins.
XX
XX Sequence 566 AA;

	Query Match	28.0%	Score 70.5:	DB 13,	Length 566:
	Best Local Similarity	32.4%:	Pred. No. 0.51:		
Matches	11: Conservative	11: Mismatches	11:	Indels	1; Gaps 1;
OY	5 RQTEBECKRQOCMQLET-SGOMRCVSOCDKREEE	37			
b	:: :: ::	:	:::::	:	:
b	39 IQGVEGCQRICESEATEEREGECGEIRREAYKE	72			

RESULT	7
ID	W40287
XX	standard; Protein; 218 AA
AC	W40287;

[illegible]

KW		Chromospondin I; melanoma; lung cancer; colon cancer;
KW		brain cancer; breast cancer.
XX		
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	Misc-difference 160	/note= "encoded by CCG"
FT	Misc-difference 161	/note= "encoded by CTC"
FT	Misc-difference 162	/note= "encoded by TGC"
FT	Misc-difference 163	/note= "encoded by AAC"
FT	Misc-difference 177	/note= "encoded by GAA"
FT	Misc-difference 178	/note= "encoded by GCG"
FT	Misc-difference 179	/note= "encoded by CGC"
PN	EP921193-A1.	
XX	09-JUN-1999.	
PF	07-JAN-1998;	98EP-0100135.
PR	05-DEC-1997;	97US-0985526.
PA	(MIXS/) MIXSON A J.	
PL	Mixson AJ;	
DR	WP1; 1999-315406/27.	
DR	N-PSDB; X58725.	
PT	Inhibition of growth of solid tumors	
PS	Disclosure; Page 17-18; 46pp; English.	
XX		
CC	This sequence represents an anti-angiogenic fragment of the thrombospondin I protein. The invention provides a carrier DNA complex that comprises DNA (see X58725-42) coding for an anti-angiogenic protein or peptide, the complex being deliverable to the site of a tumour in vivo, and which additionally comprises regulatory elements for expressing the anti-angiogenic DNA in a tumour or tumour vasculature. The complex may also include DNA encoding a tumour suppressor protein, especially p53. The carrier is a liposome, cationic polymer, micelle, microsphere, virus, viral component, or a combination of these, and administration is by intravenous or intra-tumoral injection. The complexes are useful in gene therapy for inhibition of tumour growth. The types of tumors which may be treated include solid tumors such as melanomas and tumors in the lung, colon, brain and breast.	
SQ	Sequence	218 AA;
OY	Query Match	26.6%; Score 67; DB 20; Length 218;
Dd	Best Local Similarity	39.5%; Pred.No. 0.49;
Matches	15; Conservative	6; Mismatches 11; Indels 6; Gaps 2;
13	RQCMOLE-----TSGOMRRC-VSCGDKRFEDIDMSKY 44	
11	: : : :	
104	rscdslnrcegssvqtrcthgcdckrfkdgyswshw 141	
RESULT	9	
ID	R40823 standard; protein; 239 AA.	
XX		
XC	R40823;	
XX		

DT		03-MAR-1994	(first entry)				
XX							
DE		Human thrombospondin 1.					
XX							
KW		htSP-1; platelet glycoprotein; angiogenesis; neovascularisation;					
KW		inhibitor; solid tumour; skin cancer; angiogenic dysfunction;					
KW		melanoma; diabetic retinopathy; psoriasis; neovascular glaucoma;					
KM		Kaposi's sarcoma; inflammation; retrolental fibroplasia.					
XX							
OS		Homo sapiens.					
XX							
PN		M09316716-A.					
XX							
PD		02-SEP-1993.					
XX							
PE		22-FEB-1993; 93MO-US01652.					
XX							
PR		24-FEB-1992; 92US-0841656.					
XX							
PA		(NOUN) UNIV NORTHWESTERN.					
XX							
PI		Bouck NP, Frazier WA, Good DJ, Polverini PJ;					
DR		WPL: 1993-288118/36.					
XX							
PS		Claim 10; Page 41-42; 51pp: English.					
PT		Compn. for inhibiting angiogenesis - contg. a vascularisation					
PT		inhibitor comprising a peptide capable of inhibiting					
XX		vascularisation					
CC							
CC		Certain fragments of thrombospondin, a glycoprotein found in the					
CC		alpha granules of platelets, can inhibit vascularisation. Peptides					
CC		derived from the htSP sequence are useful for inhibiting					
CC		neovascularisation, esp. in solid tumours such as melanomas. The					
CC		inhibitory peptides can also be used in other diseases involving					
CC		angiogenic dysfunction. See R40824-R40830.					
XX							
SQ		Sequence	239 AA;				
			.				
		Query Match	26.6%, Score 67; DB 14; Length 239;				
		Best Local Similarity	39.5%, Pred. No. 0.54;				
		Matches	15; Conservative	6; Mismatches	11; Indels	6; Gaps	2;
OY		13 ROCMOLE-----TSGQMRC--VSCGDKRFEEDIMSKY 44					
		: : : :					
		: : : :					
DQ		93 rtscdslmrccsgsvqrlrtchldgcckrfkdgyswsh 130					
RESULT	10						
WA0288							
ID	WA0288	standard; Protein; 441 AA.					
XX							
AC	WA0288;						
XX							
DT	18-AUG-1998	(first entry)					
XX							
DE		Human concatamerised TSPI protein.					
XX							
KW		TSPI; thrombospondin; anti-angiogenic; cationic vehicle; gene therapy;					
KW		liposome; DNA complex; tumour suppressor protein; treatment; neoplastic;					
XX		metabolic disease; concatamer; tumour.					
OS		Homo sapiens.					
OS		Synthetic.					
XX							
XX							
FH		Location/Qualifiers					
FT	Misc-difference	160					
FT	Misc-difference	/note= "encoded by CCG"					
FT	Misc-difference	221					
FT	Misc-difference	/note= "encoded by GAC"					
TT	Misc-difference	383					

FT		/note= "encoded by CCG"
FT	Region	223...227
XX		/label= intervening sequence
PN		
XX	EP819758-A2.	
XX		
PD	21-JAN-1998.	
XX		
PF	16-JUL-1997;	97EP-0112154.
XX		
PR	16-JUL-1996;	96US-0680845.
XX		
PA	(MIXS/) MIXSON A J.	
XX		
PI	Mixson AJ;	
XX		
DR	WPI: 1998-078839/08.	
XX	N-PSDB: V10494.	
XX		
PT	Complexes of DNA encoding anti-angiogenic peptide - with cationic liposome(s) or cationic polymer, useful for, e.g. gene therapy of tumours	
PT		
PS	Claim 9; Page 6-7; 47pp; English.	
XX		
CC	This protein sequence represents a concatamer of thrombospondin TSP1	
CC	which is used in a method to produce a cationic vehicle consisting	
CC	of a cationic liposome:DNA complex where the DNA encodes an	
CC	anti-angiogenic peptide or tumour suppressor protein. Such complexes are	
CC	used for treatment of neoplastic and metabolic diseases especially for	
CC	gene therapy of tumours.	
XX		
SQ	Sequence	441 AA;
OY	13	ROCQMOLE-----TSGQMRRC-VSQCDKREEDIMWSKY 44
DB	104	tscdslmrcegsyvtrtchqiecdkrfkgdgygshw 141
		26.6%; Score 67; DB 19; Length 441;
		Best local Similarity 39.5%; Pred. No. 1;
		Matches 15; Conservative 6; Mismatches 11; Indels 6; Gaps 2;
RESULT	11	
Y06183		
ID	Y06183 standard: Protein; 441 AA.	
XX		
AC	Y06183;	
XX		
DT	16-AUG-1999 (first entry)	
XX		
DE	Thrombospondin I fragment concatamer.	
XX		
KW	Anti-angiogenic; carrier:DNA complex; tumour; gene therapy; human;	
RW	thrombospondin I; melanoma; lung cancer; colon cancer;	
KW	brain cancer; breast cancer; concatamer.	
XX		
OS	Homo sapiens.	
XX		
XX		
Key	Location/Qualifiers	
FT	Misc-difference 33	/note= "encoded by GAT"
FT	Misc-difference 34	/note= "encoded by GAT"
FT	Misc-difference 81	/note= "encoded by GAT"
FT	Misc-difference 81	/note= "encoded by GAT"
FT	Misc-difference 82	/note= "encoded by GAT"
FT	Misc-difference 97	/note= "encoded by TGG"
FT	Misc-difference 97	/note= "encoded by AAT"
FT	Misc-difference 98	/note= "encoded by GCA"
FT		

FT Misc-difference 160 /note= "encoded by CGC"
 FT Misc-difference 383 /note= "encoded by CGC"
 FT Misc-difference 383 /note= "encoded by CGC"
 XX
 PN EP921193-A1.
 XX
 PD 09-JUN-1999.
 XX
 PF 07-JAN-1998; 98EP-0100135.
 XX
 PR 05-DEC-1997; 97US-0985526.
 XX
 PA (MIXS/) MIXSON A J.
 XX
 PI Mixson AJ;
 XX
 DR WPI: 1999-315406/27.
 DR N-PSDB: X58726.
 XX
 PT Inhibition of growth of solid tumors
 XX
 PS Disclosure; Page 19-20; 46pp; English.
 XX
 CC The present sequence represents a concatamer of anti-angiogenic
 CC fragments of thrombospondin I. The invention provides a carrier:DNA
 CC complex that comprises DNA (see X58725-42) encoding at least one
 CC anti-angiogenic protein or peptide, the complex being deliverable
 CC to the site of a tumor in vivo, and additionally comprises
 CC regulatory elements for expressing the anti-angiogenic DNA in a
 CC tumour or tumour vasculature. The complex may also include DNA
 CC encoding a tumour suppressor protein, especially p53. The carrier
 CC is a liposome, cationic polymer, micelle, microsphere, virus, viral
 CC component, or a combination of these, and administration is by
 CC intravenous or intratumoral injection. The complexes are useful in
 CC gene therapy for inhibition of tumour growth. The types of tumors
 CC which may be treated include solid tumors such as melanomas and
 CC tumors in the lung, colon, brain and breast. Use of concatamers
 CC can increase the anti-angiogenic dosage level without altering the
 CC amount of vector necessary for delivery.
 CC
 SQ Sequence 441 AA;
 XX
 Query Match 26.6%; Score 67; DB 20; Length 441;
 Best Local Similarity 39.5%; Pred. No. 1;
 Matches 15; Conservative 6; Mismatches 11; Indels 6; Gaps 2;
 QY 13 ROCMOLE-----TSGOMRC-VSQCCKRFEEDIDMSKY 44
 Db 104 rscdslnmrcgssvgtlchqcdkrfkqdgwshw 141
 XX
 RESULT 12
 W90340
 ID W90340 standard; protein: 444 AA.
 XX
 AC W90340;
 XX
 DT 24-MAY-1999 (first entry)
 XX
 DE G. max truncated SBP1 protein.
 XX
 KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
 KM seed; carbohydrate content; soybean.
 XX
 OS Glycine max.
 XX
 PN WO9853086-A1.
 XX
 PD 26-NOV-1998.
 XX
 PF 21-MAY-1998; 98WO-US10465.
 XX
 PR 21-MAY-1998; 98WO-US10465.

XX
 PR 22-MAY-1997; 97US-0047568.
 XX
 PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
 XX
 PI Chao WS, Grimes HD;
 XX
 DR WPI: 1999-070155/06.
 XX
 PT New modified plant sucrose binding proteins - used to develop
 PT transgenic plants which can have enhanced or decreased sucrose
 PT uptake activity in developing seeds
 XX
 PS Claim 7; Page 36-37; 58pp; English.
 XX
 CC This sequence represents a novel sucrose binding protein, SBP1 isolated
 CC from Glycine max. This protein is used in a method resulting in the
 CC production of a modified plant sucrose binding protein (SBP) which has a
 CC modified amino acid sequence compared to a corresponding wild-type SBP,
 CC and where expression of the modified SBP in a yeast assay system confers
 CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
 CC The products of the invention can be used for producing transgenic plants
 CC which have modified sucrose uptake activity, particularly in developing
 CC seeds. Enhanced sucrose uptake activity in developing seeds may be
 CC desirable where it is an advantage to increase the carbohydrate content
 CC of the seed (e.g. where the seed is the primary plant material harvested,
 CC such as soybean). In contrast, decreased sucrose uptake activity in
 CC seeds might be desirable where the vegetative material of the plant is
 CC harvested. The SBP regulatory regions confer specific or enhanced
 CC expression in developing seeds and so may be used to express any
 CC transgene in developing seeds.
 CC
 SQ Sequence 444 AA;
 XX
 Query Match 25.0%; Score 63; DB 20; Length 444;
 Best Local Similarity 38.2%; Pred. No. 3.3;
 Matches 13; Conservative 4; Mismatches 15; Indels 2; Gaps 1;
 QY 2 EFDROEYEECKROCMOLE--TSGOMRCVSCDK 33
 Db 34 eedpelpvltchqcgqgqytegdkrvclqscdr 67
 XX
 RESULT 13
 W90339
 ID W90339 standard; protein: 524 AA.
 XX
 AC W90339;
 XX
 DT 24-MAY-1999 (first entry)
 XX
 DE G. max SBP1 protein.
 XX
 KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
 KM seed; carbohydrate content; soybean.
 XX
 OS Glycine max.
 XX
 PN WO9853086-A1.
 XX
 PD 26-NOV-1998.
 XX
 PF 21-MAY-1998; 98WO-US10465.
 XX
 PR 22-MAY-1997; 97US-0047568.
 XX
 PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
 XX
 PI Chao WS, Grimes HD;
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 DR WPI: 1999-070155/06.
 XX

PT New modified plant sucrose binding proteins - used to develop
PT transgenic plants which can have enhanced or decreased sucrose
PT uptake activity in developing seeds

PS Disclosure; Page 34-36; 58pp; English.

XX This sequence represents a novel sucrose binding protein, SBP1 isolated
CC from glycine max. This protein is used in a method resulting in the
CC production of a modified plant sucrose binding protein (SBP) which has a
CC modified amino acid sequence compared to a corresponding wild-type SBP,
CC and where expression of the modified SBP in a yeast assay system confers
CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
CC The products of the invention can be used for producing transgenic plants
CC which have modified sucrose uptake activity, particularly in developing
CC seeds. Enhanced sucrose uptake activity in developing seeds may be
CC desirable where it is an advantage to increase the carbohydrate content
CC of the seed (e.g. where the seed is the primary plant material harvested,
CC such as soybean). In contrast, decreased sucrose uptake activity in
CC seeds might be desirable where the vegetative material of the plant is
CC harvested. The SBP regulatory regions confer specific or enhanced
CC expression in developing seeds and so may be used to express any
CC transgene in developing seeds.

XX Sequence 524 AA:

SQ

Query Match 25.0%; Score 63; DB 20; Length 524;
Best Local Similarity 38.2%; Pred. NO. 3.9'
Matches 13; Conservative 4; Mismatches 15; Indels 2; Gaps 1;

OY 2 EFDROEYEBCKRQCQMOL--TSGQMRRCVSGCDK 33
I : I I I I I : I I I I I :
Db 34 eeedpelvtckhqcgqgyltegdrrvcldsqcdr 67

RESULT 14
W90342 W90342 standard; protein; 409 AA.
ID ID
AC AC
XX XX
XX W90342:
DT 24-MAY-1999 (first entry)
DE G. max truncated SBP2 protein.
XX XX
KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
KM seed; carbohydrate content; soybean.
XX OS Glycine max.
XX OS
XX PN WO9853086-A1.
XX PD 26-NOV-1998.
XX PE 21-MAY-1998; 98WO-US10465.
XX PR 22-MAY-1997; 97US-0047568.
XX PA (UNIM) UNIV WASHINGTON STATE RES FOUND.
XX PI Chao WS, Grimes HD;
XX DR WPI; 1999-070155/06.
XX WPI; 1999-070155/06.

PT New modified plant sucrose binding proteins - used to develop
PT transgenic plants which can have enhanced or decreased sucrose
PT uptake activity in developing seeds

PS Claim 7; Page 39-40; 58pp; English.

XX This sequence represents a novel sucrose binding protein, SBP2 isolated
CC from glycine max. This protein is used in a method resulting in the
CC production of a modified plant sucrose binding protein (SBP) which has a
CC modified amino acid sequence compared to a corresponding wild-type SBP,
CC and where expression of the modified SBP in a yeast assay system confers
CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
CC The products of the invention can be used for producing transgenic plants
CC which have modified sucrose uptake activity, particularly in developing
CC seeds. Enhanced sucrose uptake activity in developing seeds may be
CC desirable where it is an advantage to increase the carbohydrate content
CC of the seed (e.g. where the seed is the primary plant material harvested,
CC such as soybean). In contrast, decreased sucrose uptake activity in
CC seeds might be desirable where the vegetative material of the plant is
CC harvested. The SBP regulatory regions confer specific or enhanced
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CC transgene in developing seeds.

CC	modified amino acid sequence compared to a corresponding wild-type SBP,
CC	and where expression of the modified SBP in a yeast assay system confers
CC	enhanced sucrose uptake compared to the corresponding wild-type SBP.
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CC	seeds. Enhanced sucrose uptake activity in developing seeds may be
CC	desirable where it is an advantage to increase the carbohydrate content
CC	of the seed (e.g. where the seed is the primary plant material harvested,
CC	such as soybean). In contrast, decreased sucrose uptake activity in
CC	seeds might be desirable where the vegetative material of the plant is
CC	harvested. The SBP regulatory regions confer specific or enhanced
CC	expression in developing seeds and so may be used to express any
CC	transgene in developing seeds.
SQ	
XX	Sequence 409 AA:
XX	
XX	
Query Match	24.8%; Score 62.5; DB 20; Length 409;
Best local Similarity	36.6%; Pred. No. 3.5;
Matches 15; Conservative 3; Mismatches 14; Indels 9; Gaps 2	
OY	7 EYECKROCMOLE--TSGQMRRVCVSCD-----KRFEPD 38
Dd	: :
	38 elvtckhgccqqrtyresdkrtcltgcqcdsmkgerexqeese 78
RESULT 15	
W90341	
ID	W90341 standard; protein: 489 AA.
AC	W90341;
XX	
DT	24-MAY-1999 (first entry)
XX	
DE	G. max SBP2 protein.
XX	
KM	SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
KW	seed; carbohydrate content; soybean.
XX	
OS	Glycine max.
XX	
PN	WO9853086-A1.
PD	26-NOV-1998.
PF	21-MAY-1998; 98MO-US10465.
PR	22-MAY-1997; 97US-0047568.
XX	
PA	(UNITM) UNIV WASHINGTON STATE RES FOUND.
XX	
PI	Chao WS, Grimes HD;
DR	WPI; 1999-070155/06.
PT	
PT	New modified plant sucrose binding proteins - used to develop
PT	transgenic plants which can have enhanced or decreased sucrose
PT	uptake activity in developing seeds
XX	
PS	Claim 13b; Page 37-38; 58pp; English.
XX	
CC	This sequence represents a novel sucrose binding protein, SBP2 isolated
CC	from glycine max. This protein is used in a method resulting in the
CC	production of a modified plant sucrose binding protein (SBP) which has a
CC	modified amino acid sequence compared to a corresponding wild-type SBP,
CC	and where expression of the modified SBP in a yeast assay system confers
CC	enhanced sucrose uptake compared to the corresponding wild-type SBP.
CC	The products of the invention can be used for producing transgenic plants
CC	which have modified sucrose uptake activity, particularly in developing
CC	seeds. Enhanced sucrose uptake activity in developing seeds may be
CC	desirable where it is an advantage to increase the carbohydrate content
CC	of the seed (e.g. where the seed is the primary plant material harvested,
CC	such as soybean). In contrast, decreased sucrose uptake activity in

